



Fig. 4. Spike count matched model. Spike trains are generated so that there is one simulated spike train to match each train in the data, with the spike count in the simulated train being forced to be equal to the corresponding train in the data. The top panel shows the average spike density plot for the responses of one V1 supragranular complex cell aligned at the time of stimulus onset. This is integrated over the whole period to give the curve in the lower panel. This integrated spike probability density function is then used to generate simulated spike trains using a uniform random number generator. The number of spikes needed is chosen from the number of spikes in the recorded data. In this example, six spikes were needed, so six random numbers would be chosen, placed on the ordinate and mapped through the cumulative spike density function as shown to generate the simulated spike train indicated by the dots at the bottom. For illustration here, six numbers separated by equal intervals were used. After transformation through the cumulative probability function the intervals are no longer equal. Using this procedure places the spikes stochastically due to the random numbers. However, the probability density function averaged across many examples will be indistinguishable from that in the upper panel.